

**Appl. No.** : 09/539,032  
**Filed** : March 30, 2000

### **REMARKS**

Claim 1 has been amended to correct a typographical error. Thus, claims 1-4 and 6-9 remain pending in the present application. No new matter has been added. Reconsideration and withdrawal of the present rejection in view of the comments presented herein are respectfully requested.

#### Interview summary

The undersigned would like to thank Examiner Clow for the courtesy extended to him during the telephonic interview conducted on July 13, 2009. The substance of this interview is incorporated into the amendment and remarks presented herein.

#### Rejection under 35 U.S.C. § 112, first paragraph

Claims 1-4 and 6-9 were rejected under 35 U.S.C. § 112, first paragraph as allegedly failing to comply with the written description requirement. In particular, the Examiner contends that the recitation at step iii) of “computationally matching using one or more computer processors the sorted peptide sequences of length ‘N’ of the selected pathogenic organisms to produce exactly matched common peptide sequences using a peptide library matching software program (PEMLIMP)” is new matter.

The Examiner points to the specification at page 5 which teaches that PEPLIMP is a program which compares the peptide libraries of organisms selected by a user. As noted during the telephonic interview, the specification at page 14, Example 2 (which describes the PEPLIMP program), teaches that “The purpose of the program is to compare the user defined peptide libraries with each other and report the common/unique peptides. The output files of the program PEPLIB are used as input for the PEPLIMP program.” Thus, comparing user defined peptides with each other clearly involves a computational matching process of the peptide sequences to produce exactly matched common peptide sequences. The Examiner agreed that this disclosure is sufficient support for the “computationally matching” language in claim 1, step iii).

In addition, as shown in Example 1, the output of the PEPLIB program comprises an alphabetically sorted peptide library as noted at the top of page 14 of the specification (The

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output file). Thus, the PEPLIMP uses these sorted peptide libraries to compare (match) and report common, exactly matched peptides (as noted schematically in Fig.1, diamond-shaped box in which Peptide (i)=Peptide (j)). Thus, the language recited in claim 1, step iii) is fully supported by the specification, and does not constitute new matter.

In view of the comments presented above, Applicants respectfully request reconsideration and withdrawal of the rejection under 35 U.S.C. § 112, first paragraph.

### CONCLUSION

Applicants submit that all claims are in condition for allowance. If any issues remain that could be resolved by telephone, the Examiner is cordially invited to contact the undersigned at the telephone number provided below. Please charge any additional fees, including any fees for additional extension of time, or credit overpayment to Deposit Account No. 11-1410.

Respectfully submitted,

KNOBBE, MARTENS, OLSON & BEAR, LLP

Dated: 8/11/09

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